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QY 301 KLEETLEEOQRQKROGQGMFRKAKPEQIRAIISOQATSPRRGGERLAINLLSQSPYIS 360  
Db 361 NONGRFFEACEDFESQFQNMNDVAVSAFKLNOGALFVPHYNSKATFVVTGIGYQAOMAC 420  
QY 361 NONGRFFEACEDFESQFQNMNDVAVSAFKLNOGALFVPHYNSKATFVVTGIGYQAOMAC 420  
Db 361 NONGRFFEACEDFESQFQNMNDVAVSAFKLNOGALFVPHYNSKATFVVTGIGYQAOMAC 420  
QY 421 PHLSROGSGSGRODRRODEESEEETFEFGFOVKAPLSPGDVFVAPAGHAATFFASKD 480  
Db 421 PHLSROGSGSGRODRRODEESEEETFEFGFOVKAPLSPGDVFVAPAGHAATFFASKD 480  
QY 421 PHLSROGSGSGRODRRODEESEEETFEFGFOVKAPLSPGDVFVAPAGHAATFFASKD 480  
Db 481 QPLNAVAFGLNAQNNQRIIFLAGRPFELNHKONTNVIKFTVASAY 525  
QY 481 QPLNAVAFGLNAQNNQRIIFLAGRPFELNHKONTNVIKFTVASAY 525  
RESULT 2  
ID R20181 standard: Protein; 566 AA.  
AC R20181:  
DT 16-APR-1992 (first entry)  
DE Sequence encoded by 67 kd T. cacao protein cDNA.  
KW Cocoa; flavour; vicillin; seed storage protein.  
OS Theobroma cacao.  
PN M09119801-A.  
PD 26-DEC-1991.  
PE 07-JUN-1991; G00914.  
PR 11-JUN-1990; GB-013016.  
PA (MRS) MARKS UK LTD.  
PI Spencer ME, Hodge R, Deakin EA, Ashton S;  
DR WPI: 92-024418/03.  
DR N-PSDB: 020377.  
PT Recombinant cocoa proteins - are responsible for flavour in cocoa  
beans and produced in large quantities using yeast and bacterial  
expression vectors  
PS Claim 4: Fig 2: 59pp: English.  
CC The inventors claim a 67 kd and 31 kd T. cacao protein, and  
CC fragments, and encoding DNAs. The 47 kd and 31 kd proteins are  
CC derived from the 67 kd precursor. T. cacao protein cDNA was  
CC detected in a cDNA library prepared from immature cocoa beans RNA  
CC using a probe based on the AA sequence of a CNBR peptide common to  
CC the 47 kd and 31 kd polypeptides. Homology searches revealed close  
CC homologies between the 67 kd polypeptide and the vicillins, which are  
CC seed storage proteins.  
SQ Sequence 566 AA:  
Query Match 96.0%; Score 3654; DB 1; Length 566;  
Best Local Similarity 96.7%; Pred. No. 0.00e+00;  
Matches 504; Conservative 10; Mismatches 6; Indels 1; Gaps 1;

Db 361 NONGRFFEACEDFESQFQNMNDVAVSAFKLNOGALFVPHYNSKATFVVTGIGYQAOMAC 420  
QY 361 NONGRFFEACEDFESQFQNMNDVAVSAFKLNOGALFVPHYNSKATFVVTGIGYQAOMAC 420  
Db 421 PHLSROGSGSGRODRRODEESEEETFEFGFOVKAPLSPGDVFVAPAGHAATFFASKD 480  
QY 421 PHLSROGSGSGRODRRODEESEEETFEFGFOVKAPLSPGDVFVAPAGHAATFFASKD 480  
Db 481 QPLNAVAFGLNAQNNQRIIFLAGRPFELNHKONTNVIKFTV 520  
QY 481 QPLNAVAFGLNAQNNQRIIFLAGRPFELNHKONTNVIKFTV 520

RESULT 3  
ID W62832 standard: Protein; 590 AA.  
AC W62832;  
DT 27-OCT-1998 (first entry)  
DE Gossypium hirsutum antimicrobial protein.  
KW antimicrobial protein; Infestation; control.  
OS Gossypium hirsutum.  
PN W09827805-A1.  
PD 02-JUL-1998.  
PE 22-DEC-1997; AU0874.  
PR 20-DEC-1996; AU-004275.  
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.  
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;  
DR WPI: 98-377279/32.  
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -  
PT useful for controlling microbial infestations of plants or mammals  
PS Claim 1: Page 49-51: 96pp; English.  
CC The sequence is that of an antimicrobial protein which can  
CC be used to control microbial infestations in plants and mammalian  
CC animals.  
SQ Sequence 590 AA:

Query Match 50.2%; Score 1910; DB 1; Length 590;  
Best Local Similarity 50.9%; Pred. No. 7.10e-157;  
Matches 261; Conservative 95; Mismatches 92; Indels 11; Gaps 10;

Db 82 DPGRRYECCQEC-RQ-EBRQOPQCCQRLKRF-EGE-QQGS--QRFQECQCHQOE 135  
QY 37 DPGRRYECCQEC-RQ-EBRQOPQCCQRLKRF-EGE-QQGS--QRFQECQCHQOE 96  
Db 136 QRPBKQOCVRECEKRYQENPMRGEREE-BAEED-TEEGEODSHNPFHF-RSFSQR 192  
QY 97 QGOREQOCCQKCEQYKEQE-RGEHENYHNHKKRNEEGQORNNPYFPKRRSFQTR 155  
Db 193 FREDHGNFVLRASHNPLIRGINERLSILANPRTFVLRPHHCAEKIYLTNGRGL 252  
QY 156 FREDHGNFVLRASHNPLIRGINERLSILANPRTFVLRPHHCAEKIYLTNGRGL 215  
Db 253 TFLHHEKESYNIAPGVVAVPAGSTVYLANQNKELIAVLHPRVNNNGOFEFFPAG 312  
QY 216 TFLHHEKESYNIAPGVVAVPAGSTVYLANQNKELIAVLHPRVNNNGOFEFFPAG 275  
Db 313 SORPQSLRAFREILPATNTRSEQIDELFGQRSHRRQGG-GWFRKASQDQIRALSQ 371  
QY 276 NKRPESTYGAFSYVLETVENTOREKLEETLEFQROKROGQGMFRKAKPEQIRAI 335  
Db 372 EATSPRKSERAFANLNLSTPRYSNONGFRFFACRPFEPQLDINDIVYALDLONGSTF 431  
QY 336 QATSPRKSERAFANLNLSTPRYSNONGFRFFACRPFEPQLDINDIVYALDLONGSTF 395  
Db 432 VPHYNSKATFVVTGIGYQAOMACPHLSROGSGSGRODRRODEESEEETFEFGFOY 491  
QY 396 VPHYNSKATFVVTGIGYQAOMACPHLSROGSGSGRODRRODEESEEETFEFGFOY 455  
Db 492 RSRLSRGDIFFVAPNPVTFVASONLRLMTGGLYNON 530  
QY 456 KAPLSPGDVFVAPAGHAATFFASKDQPLNAVAFGLNAQNN 494

RESULT 4

ID	W62829	standard; Protein; 666 AA.
AC	W62829	
DT	27-OCT-1998	(first entry)
DE	Macadamia integrifolia antimicrobial protein.	
KW	antimicrobial protein; infestation; control.	
OS	Macadamia integrifolia.	
FT	Key	Location/Qualifiers
FT	Peptide	1..28
FT		/note="signal peptide"
FT	Protein	29..666
FT		/note="mature protein"
PN	W09827805-A1.	
PD	02-JUL-1998.	
PF	22-DEC-1997.	AU0874.
PR	20-DEC-1996:	AU-004275.
PA	(RERTR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.	
PI	Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;	
DR	WPI: 98-377279/32.	
DR	N-PSDB: V42311.	
DT	Novel anti-microbial protein from e.g. Macadamia integrifolia -	
PT	useful for controlling microbial infestations of plants or mammals	
PS	Claim 1; Page 39-41; 96pp; English.	
CC	The sequence is that of an antimicrobial protein which can	
CC	be used to control microbial infestations in plants and mammalian	
CC	animals.	
Sequence	666 AA;	
50		

Query Match	31.3%	Score 1193	DB 1	Length 666
Best Local Similarity	40.6%	Pred. 1,188	-92	
Matches 195	Conservative 122	Mismatches 140	Indels 23	Gaps 17
Db	135	RHLEPRNH-OTCOQCEERLEYEKRRQQRKYEEQOEDEDEKYEERKEEDNRDPQRE	193	
QY	33	QYEDRPQOYEQOCCRESE--ATEEEOE--QCE--QCEER--YKQORQOE--E--LQRQ	84	
Db	194	YEDRRRC-EEQO--PROYOQCRRCQOQOHGQGDILMPORGSGSGRYEEGEKSDNP	251	
QY	85	YQCGGCGEQEQOQOQRRQOQOQKRCWQYKEQENG--EHENYHNHKKRSEEGEQRRNP	143	
Db	252	YVEDR--SLSTFETEEGHISVLENFYGRSKLLRLAKNRYLVLEAPNPAFVLPFLDAD	310	
QY	144	YYPEKRSFQTRFEEDEGNFKILQREFANSPPLKGINDYRLAMEAPNPFILPHQDAE	203	
Db	311	ALLVTRGRLKMIHNDRESYVLECGDVIRIPAGTFEYLINRDNERRTIKFLQTS	370	
QY	204	AIYVTNGKGTITVTEKNESINWQGYVSPAGSTVYVSDNNQKLTILVLLPVP	263	
Db	371	TPGOYKEFFPAGGNPEPVLSTFSKELLEALNTQAEIRLGLVGLQOREGYIASQEOIR	430	
QY	264	SPGYELFFPAGNNKPESYGAESYEVLEFVFNOREKLEIIEORGQRQOQOGMFP	323	
Db	431	ELTRDD--SSRRMHIRGESSGPNLEFNKRPVRSNKGOAYEYKPEPYRLODMVDS	488	
QY	324	KAKEQIRALISQATSPRRHNGERLAINLISQSPVYSNONGREFEACPEDFSQFMMDDA	383	
Db	489	VFLANITQGSNMGPEFNTSTKYVVVYASGEADYEMACPRLSGR--HGRRG--GKR--HEEE	544	
QY	384	VSAFKLMOGAIFFPHYNSKATFVFVFDGTYQMCMCPHLSRQSGSGSQRDRQOEER	443	
Db	545	--EDV--HYEDQYRLKREAIYVPHVPVAFVSSGNEILLAFGINQNNHENTLAGR	600	
QY	444	SEETFEFEOQYKRLPSGDVYFAPAGHATFFASKDQPLNAVAYGLNMQNRITLAGR	503	
RESULT	5			
ID	W62828	standard; Protein; 666 AA.		
AC	W62828			
DT	27-OCT-1998	(first entry)		
DE	Macadamia integrifolia antimicrobial protein.			
KW	antimicrobial protein; Infestation; control.			
OS	Macadamia integrifolia.			
FT	key			
FT	Peptide	Location/Qualifiers		
		1..28		

FT	Protein	/note="signal peptide"
FT		29, 666
PT		/note="mature protein"
PN	W09827805-A1.	
PD	02-JUL-1998.	
PF	22-DEC-1997; AU0874.	
PR	20-DEC-1996; AU-004275.	
PA	(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.	
PI	Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;	
DR	WPI: 98-377279/32.	
DR	N-PSDB: V42310.	
PT	Novel anti-microbial protein from e.g. <i>Macadamia integrifolia</i> -	
PT	useful for controlling microbial infestations of plants or mammals	
PS	Claim 1; Page 34-36; 96pp; English	
CC	The sequence is that of an anti-microbial protein which can	
CC	be used to control microbial infestations in plants and mammalian	
CC	animals.	
CC	Sequence	666 AA;
50		

[illegible]







Db 148 TFSVPRHFDSEVLEFNKRAVLGLVRESETEKITLEPGDMIHIPAGTPLYVNRDENEX 207  
 193 TFLPHHCDAEALFYVNGKGTITFTVHENKESYVQRGTVSVAPASTVYVSQDNOEK 252  
 QY 208 LLLAMLHIVSTGKEEFEEFGGGRDPESVLSAFSNNVLAALQTPKGLERLEN-O-Q 264  
 253 LTTAVALPVPNSPKYELFFPAGNNKPEESYGAFSYEVLFTVETOREKLEETLEEDRGQ 312  
 QY 265 N--EG--SIFKISR-ERVALAPTKKSSWMPFGESKAOFNIFSKRPFNGYGRLEEVG 319  
 313 KROQGQGMFRKRAKPPQIRAIISOATSPRRH-GGE-RLAINLSQSPVSNQNGRFEAC 370  
 Db 320 PDDEKSWLQRLNMLTFTNTQSMSTIHYNSHATKIALVMDGRGHLQISCPHMS--SR- 376  
 371 PEDFSQ-FQNMDDVAVSAFLNQCAGIFVPHYNSKATFVFTDGYGAQMACPHLSRQSG 429  
 QY 377 SDS-KHDKS-----P-S-YHRISADLKPGVFFVPPGHPVTTASKENLITICE 425  
 430 SOSGRQDRROEESSEETFGFQVAKAPLSPGDVFAVAPAGHATFFASKDQPLNAVAFG 489  
 Db 426 VNVDRNKRTFAGK 439  
 QY 490 LMAONNRITLAGR 503

RESULT 13  
 ID W90342 standard; protein; 409 AA.  
 AC W90342;  
 DT 24-MAY-1999 (first entry)  
 DE G. max truncated SBP2 protein.  
 KM SBP1: sucrose binding protein; SBP2: sucrose uptake; transgenic plant;  
 KW seed; carbohydrate content; soybean.  
 GN Glycine max.  
 PN WO9853086-A1.  
 PD 26-NOV-1998.  
 PF 21-MAY-1998: U10465.  
 PR 22-MAY-1997: US-047568.  
 PA (UNITV) UNIV WASHINGTON STATE RES FOUND.  
 PI Chao WS, Grimes HD;  
 DR WPI: 99-070155/06.  
 PT New modified plant sucrose binding proteins - used to develop  
 transgenic plants which can have enhanced or decreased sucrose  
 uptake activity in developing seeds  
 PS Claim 7: Page 39-40; 58pp; English.  
 CC This sequence represents a novel sucrose binding protein (SBP) isolated  
 from glycine max. This protein is used in a method resulting in the  
 production of a modified plant sucrose binding protein (SBP) which has a  
 modified amino acid sequence compared to a corresponding wild-type SBP,  
 and where expression of the modified SBP in a yeast assay system confers  
 enhanced sucrose uptake compared to the corresponding wild-type SBP.  
 CC The products of the invention can be used for producing transgenic plants  
 CC which have modified sucrose uptake activity, particularly in developing  
 CC seeds. Enhanced sucrose uptake activity in developing seeds may be  
 CC desirable where it is an advantage to increase the carbohydrate content  
 CC of the seed (e.g. where the seed is the primary plant material harvested,  
 CC such as soybean). In contrast, decreased sucrose uptake activity in  
 CC seeds might be desirable where the vegetative material of the plant is  
 CC harvested. The SBP regulatory regions confer specific or enhanced  
 CC expression in developing seeds and so may be used to express any  
 CC transgene in developing seeds.  
 CC Sequence 409 AA.

Query Match 19.0%; Score 724; DB 1; Length 409;  
 Best Local Similarity 32.6%; Pred. No. 7,49e-51;  
 Matches 118; Conservative 114; Mismatches 116; Indels 14; Gaps 11;

Db 29 KETFEVDEDELVTCKHQQOQOQRTSDKFTCLQOC-DSNKOERQVVEETKEKEEHO 87  
 75 ROOEELFQRYOQOCGRCEQOQ-GOREQOQOCRKCEYK-EOERHEHNYHNHKKNS 122  
 QY 88 EOHHEEEDENPVYFEEDKXSTRVETEGGSIRVLKFTKESKILQGENRLAILARAH 147  
 133 EEEEGOQNNPYPFKRRSFOTFRDEEGNFKLQRFAPENSPLKGINDRILAMFAPNP 192

Db 148 TFSVPRHFDSEVLEFNKRAVLGLVRESETEKITLEPGDMIHIPAGTPLYVNRDENEX 207  
 193 TFLPHHCDAEALFYVNGKGTITFTVHENKESYVQRGTVSVAPASTVYVSQDNOEK 252  
 QY 208 LLLAMLHIVSTGKEEFEEFGGGRDPESVLSAFSNNVLAALQTPKGLERLEN-O-Q 264  
 253 LTTAVALPVPNSPKYELFFPAGNNKPEESYGAFSYEVLFTVETOREKLEETLEEDRGQ 312  
 QY 265 N--EG--SIFKISR-ERVALAPTKKSSWMPFGESKAOFNIFSKRPFNGYGRLEEVG 319  
 313 KROQGQGMFRKRAKPPQIRAIISOATSPRRH-GGE-RLAINLSQSPVSNQNGRFEAC 370  
 Db 320 PDDEKSWLQRLNMLTFTNTQSMSTIHYNSHATKIALVMDGRGHLQISCPHMSRSDS 379  
 371 PEDFSQ-FQNMDDVAVSAFLNQCAGIFVPHYNSKATFVFTDGYGAQMACPHLSRQSG 429  
 QY 380 KH 381  
 430 SQ 431

RESULT 14  
 ID W90339 standard; protein; 524 AA.  
 AC W90339;  
 DT 24-MAY-1999 (first entry)  
 DE G. max SBP1 protein.  
 KM SBP1: sucrose binding protein; SBP2: sucrose uptake; transgenic plant;  
 KW seed; carbohydrate content; soybean.  
 GN Glycine max.  
 PN WO9853086-A1.  
 PD 26-NOV-1998.  
 PF 21-MAY-1998: U10465.  
 PR 22-MAY-1997: US-047568.  
 PA (UNITV) UNIV WASHINGTON STATE RES FOUND.  
 PI Chao WS, Grimes HD;  
 DR WPI: 99-070155/06.  
 PT New modified plant sucrose binding proteins - used to develop  
 transgenic plants which can have enhanced or decreased sucrose  
 uptake activity in developing seeds  
 PS Disclosure: Page 34-36; 58pp; English.  
 CC This sequence represents a novel sucrose binding protein, SBP1 isolated  
 from glycine max. This protein is used in a method resulting in the  
 production of a modified plant sucrose binding protein (SBP) which has a  
 modified amino acid sequence compared to a corresponding wild-type SBP,  
 and where expression of the modified SBP in a yeast assay system confers  
 enhanced sucrose uptake compared to the corresponding wild-type SBP.  
 CC The products of the invention can be used for producing transgenic plants  
 CC which have modified sucrose uptake activity, particularly in developing  
 CC seeds. Enhanced sucrose uptake activity in developing seeds may be  
 CC desirable where it is an advantage to increase the carbohydrate content  
 CC of the seed (e.g. where the seed is the primary plant material harvested,  
 CC such as soybean). In contrast, decreased sucrose uptake activity in  
 CC seeds might be desirable where the vegetative material of the plant is  
 CC harvested. The SBP regulatory regions confer specific or enhanced  
 CC expression in developing seeds and so may be used to express any  
 CC transgene in developing seeds.  
 CC Sequence 524 AA.

Query Match 18.4%; Score 702; DB 1; Length 524;  
 Best Local Similarity 33.2%; Pred. No. 6,39e-49;  
 Matches 147; Conservative 136; Mismatches 120; Indels 40; Gaps 25;

Db 34 EEDDELVTCKHQQOQOQRTSDKFTCLQOC-DRHNRKQREKQIOETETKEEER 92  
 79 EELQRYOQOCGRCEQOQ-GOREQOQOCRKCEYK-K-EOERG-E-HENYHNHKK--K 129  
 QY 93 EEEEGOQOHEEDENPVYFEEDKXSTRVETEGGSIRVLKFTKESKILQGENRLAI 152  
 130 NSEEEEGOQ--RN-NPYFPKRRSFOTFRDEEGNFKLQRFAPENSPLKGINDRILAM 186  
 Db 153 LBARAHTEVSPRHFDSEVLEFNKRAVLGLVRESETEKITLEPGDMIHIPAGTPLYV 212



QY 187 FEANPNTFLPHHCDAAEAIYVNTNGKGTITFTYHKNKESYNORGTVSVAGSTVYVS 246  
DB 213 RDENDKLFAMLIHIPVSVSTPGKFEFFAPGGRDESVLSAFSNVLAALQTPKGLKN 272  
QY 247 QNOEKLTIAVALAPVN-S-PKYTELFPAGNNKPESYTGAFSYELVETVNTQREKLEE 304  
DB 273 VFD-Q--QN--EG--SIFRISR-EQVRLAAPTCKSSWMPFGESKQPFNFSKRPISNG 324  
QY 305 ILEEQGQKROOGQOGMFRKAKPEQIRAIISOATSPRRH-R-FLAINLLSQSPVYSNQ 362  
DB 325 YGRLFEVGPDDDEKSWLQRLNMLFTNTIORSMTIHYNSHATKIALYIDGRHLOJSC 384  
QY 363 NGRFFACPEDEFSQ--FQNMVAVSAFKLNOGALFVPHYNSKATFEVFTDGTGYAQMAG 420  
DB 385 PHMS--SRSSHS-KHDS-----S---P-S-YHRISSDKPGMVFVPPGHPFVITASNK 431  
QY 421 PHLSRQSGQSGQSGORRRQGESESEETFGFQGVAKAPLSPGVFVAPAGHAVTFASMD 480  
DB 432 ENILMICEVNAKDKNKFTFACK 454  
QY 481 OPLNAVAFGLNMQNORIFLAGR 503

## RESULT 15

ID W90340 standard; protein: 444 AA.  
AC W90340;  
DT 24-MAY-1999 (first entry)  
DE G. max truncated SBP1 protein.  
KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;  
KW seed; carbohydrate content; soybean.  
OS Glycine max.  
PN W09653086-R1.  
PD 26-NOV-1998.  
PE 21-MAY-1998; U10465.  
PR 22-MAY-1997; US-047568.  
PA (UNITW) UNIV WASHINGTON STATE RES FOUND.  
PI Chao WS, Gimes HD;  
PI WPI; 99-070135/06.  
PT New modified plant sucrose binding proteins - used to develop  
PT transgenic plants which can have enhanced or decreased sucrose  
PT uptake activity in developing seeds  
PS Claim 7; Page 36-37; 58pp; English.  
CC This sequence represents a novel sucrose binding protein, SBP1 isolated  
CC from Glycine max. This protein is used in a method resulting in the  
CC production of a modified plant sucrose binding protein (SBP) which has a  
CC modified amino acid sequence compared to a corresponding wild-type SBP,  
CC and where expression of the modified SBP in a yeast assay system confers  
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.  
CC The products of the invention can be used for producing transgenic plants  
CC which have modified sucrose uptake activity, particularly in developing  
CC seeds. Enhanced sucrose uptake activity in developing seeds may be  
CC desirable where it is an advantage to increase the carbohydrate content  
CC of the seed (e.g. where the seed is the primary plant material harvested,  
CC such as soybean). In contrast, decreased sucrose uptake activity in  
CC seeds might be desirable where the vegetative material of the plant is  
CC harvested. The SBP regulatory regions confer specific or enhanced  
CC expression in developing seeds and so may be used to express any  
CC transgene in developing seeds.  
SQ Sequence 444 AA;

Query Match 17.9%; Score 680; DB 1; Length 444;

Best Local Similarity 33.9%; Pred. No. 5, 41e-47;

Matches 126; Conservative 114; Mismatches 104; Indels 28; Gaps 20;

DB 34 EEDDELVTCKHQCOCQOQOYTGDKRVCLQSC-DRYHRMKORREKQIOETREKKEESR 92  
QY 79 EELQROYQCCGRCRQDEQD-GQREQOQCCQKCKWEQ-K-EQERG-E-HENYHNK---K 129  
DB 93 EREDEQOEHEBODENPYTFEEDKDFETRVETEGGRIRVLKFKTEKSKLQCIENFRLAI 152  
QY 130 NRSEEEGQO--RN-NPYFPRKRSQGTFRDEEGNFKLQRAENSPLPKGINDYRLAM 186  
DB 153 LEARAHTEVSPRHDFSEVVFENIKRAVLGLVSESETEKITLEPGDMIHIPAGTPLYIVN 212

QY 187 FEANPNTFLPHHCDAAEAIYVNTNGKGTITFTYHKNKESYNORGTVSVAGSTVYVS 246  
DB 213 RDENDKLFAMLIHIPVSVSTPGKFEFFAPGGRDESVLSAFSNVLAALQTPKGLKN 272  
QY 247 QNOEKLTIAVALAPVN-S-PKYTELFPAGNNKPESYTGAFSYELVETVNTQREKLEE 304  
DB 273 VFD-Q--QN--EG--SIFRISR-EQVRLAAPTCKSSWMPFGESKQPFNFSKRPISNG 324  
QY 305 ILEEQGQKROOGQOGMFRKAKPEQIRAIISOATSPRRH-R-FLAINLLSQSPVYSNQ 362  
DB 325 YGRLFEVGPDDDEKSWLQRLNMLFTNTIORSMTIHYNSHATKIALYIDGRHLOJSC 384  
QY 363 NGRFFACPEDEFSQ--FQNMVAVSAFKLNOGALFVPHYNSKATFEVFTDGTGYAQMAG 420  
DB 385 PHMS--SRSSHS-KH 396  
QY 421 PHLS-RQSGQSGO 431

Search completed: Sat May 13 08:27:24 2000  
Job time : 23 secs.